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FIGURE 1A

>g885075	TGCGCNGGAG	CCTGAGCGGA	GGGTGTGCGC	AGCCTCGCCA	GCGGGGGCCC
Consensus	TGCGCNGGAG	CCTGAGCGGA	GGGTGTGCGC	AGCCTCGCCA	GCGGGGGCCC
>g885075	CGGGCTGNCG	CATTGCCTCA	CTGAGCCAGC	GCCTGCCTNC	TACCTCGCCG
Consensus	CGGGCTGNCG	CATTGCCTCA	CTGAGCCAGC	GCCTGCCTNC	TACCTCGCCG
>g885075	ACAGCTGGAA	CCAGTGCAC	CTAGTGGCTC	TCACCTGCTT	CCTCCTGGGC
Consensus	ACAGCTGGAA	CCAGTGCAC	CTAGTGGCTC	TCACCTGCTT	CCTCCTGGGC
>g885075	GTGGGCTGCC	GGCTGACCCC	GGGTTTGTAC	CACCTGGGCC	GCACTGTCTT
Consensus	GTGGGCTGCC	GGCTGACCCC	GGGTTTGTAC	CACCTGGGCC	GCACTGTCTT
>g885075	CTGCATCGAC	TTCATGGTTT	TCACGGTGCG	GCTGCTTCAC	ATCTTCACGG
Consensus	CTGCATCGAC	TTCATGGTTT	TCACGGTGCG	GCTGCTTCAC	ATCTTCACGG
>g885075	TCAACAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG
>1512846	CAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG
Consensus	TCAACAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG
>g885075	GACGTGTTCT	TCTTCCTCTT	CTTCCTCGGC	GTGTGGCTGG	TAGC:TATGG
>1512846	GACGTGTTCT	TCTTCCTCTT	CTTCCTCGGC	GTGTGGCTGG	TAGCCTATGG
>1551713				C	GTGTGGCTGG
Consensus	GACGTGTTCT	TCTTCCTCTT	CTTCCTCGGC	GTGTGGCTGG	TAGCCTATGG
>g885075	GTGGGCCACG	GAGGGGT			
>1512846	CGTGGCCACG	GAGGGGCTCC	TGAGGCCACG	GGACAGTGAC	TTCCCAAGTA
>1551713	CGTGGCCACG	GAGGGGCTCC	TGAGGCCACG	GGACAGTGAC	TTCCCAAGTA
Consensus	CGTGGCCACG	GAGGGGCTCC	TGAGGCCACG	GGACAGTGAC	TTCCCAAGTA
>1512846	TCCTGCGCCG	CGTCTTCTAC	CGTCCCTACC	TGCAGATCTT	CGGGCAGATT
>1551713	TCCTGCGCCG	CGTCTTCTAC	CGTCCCTACC	TGCAGATCTT	CGGGCAGATT
>1251961					CGGGCAGATT
Consensus	TCCTGCGCCG	CGTCTTCTAC	CGTCCCTACC	TGCAGATCTT	CGGGCAGATT
>1512846	CCCCAGGAGG	ACATGGAC			
>1551713	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	GAGCACAGCA	ACTGCTCGTC
>1251961	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	GAGCACAGCA	ACTGCTCGTC
Consensus	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	GAGCACAGCA	ACTGCTCGTC
>1551713	GGAGCCCAGG	TTCTGGGCAC	ACCCTCCTGG	GGCC	
>1251961	GGAGCCCAGG	TTCTGGGCAC	ACCCTCCTGG	GGCCCAGGCG	GGCACCTGCG
Consensus	GGAGCCCAGG	TTCTGGGCAC	ACCCTCCTGG	GGCCCAGGCG	GGCACCTGCG
>1251961	TCTCCCAGTA	TGCCAACTGG	CTGGTGGTGC	TGCTCCTCGT	CATCTTCCTG
Consensus	TCTCCCAGTA	TGCCAACTGG	CTGGTGGTGC	TGCTCCTCGT	CATCTTCCTG
>1251961	CTCGTGGCCA	ACATCCTGCT	GGTCAACTTG	CTCATTGCCA	TGTTTCACTTA
Consensus	CTCGTGGCCA	ACATCCTGCT	GGTCAACTTG	CTCATTGCCA	TGTTTCACTTA
>1251961	CACATTTCGGC	AAAGTACAGG	GCAACAGCGA	TCTCTACTGG	AAGGCG
>1209763			GCGA	TCTCTACTGG	AAGGCGCAGG
Consensus	CACATTTCGGC	AAAGTACAGG	GCAACAGCGA	TCTCTACTGG	AAGGCGCAGG
>1209763	TTACCGCCTC	ATCCGGGAAT	TCCACTCTCG	GCCCGCGCTG	GCCCCGCCCT
Consensus	TTACCGCCTC	ATCCGGGAAT	TCCACTCTCG	GCCCGCGCTG	GCCCCGCCCT

U.S. PAT. 2006011111

FIGURE 1B

>1209763	TTATCGTCAT CTCCCACTTG CGCCTCCTGC TCAGGCAATT GTGCAGGCGA
Consensus	TTATCGTCAT CTCCCACTTG CGCCTCCTGC TCAGGCAATT GTGCAGGCGA
>1209763	CCCCGGAGCC CCCAGCCGTC CTCCCCGGCC CTCGAGCATT TCCGGGTTTA
Consensus	CCCCGGAGCC CCCAGCCGTC CTCCCCGGCC CTCGAGCATT TCCGGGTTTA
>1209763	CCTTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGGAA TCGGTGCATA
>1815040	GTGCATA
Consensus	CCTTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGGAA TCGGTGCATA
>1209763	AGGAGAACTT TCTGCTGGCA CG
>1815040	AGGAGAACTT TCTGCTGGCA CGCGCTAGGG ACAAGCGGGA GAGCGACTCC
Consensus	AGGAGAACTT TCTGCTGGCA CGCGCTAGGG ACAAGCGGGA GAGCGACTCC
>1815040	GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAAACAGCT
Consensus	GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAAACAGCT
>1815040	GGGACACATC CGCGAGTACG AACAGCGCCT GAAAGTGCTG GAGCGGGAGG
Consensus	GGGACACATC CGCGAGTACG AACAGCGCCT GAAAGTGCTG GAGCGGGAGG
>1815040	TCCAGCAGTG TAGCCGCGTC CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC
Consensus	TCCAGCAGTG TAGCCGCGTC CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC
>1815040	TCTGCCTTGC TGCCCCCAGG TGGGCCGCCA CCCCCTGACC TGCCTGGGTC
>1859374	GGGTC
Consensus	TCTGCCTTGC TGCCCCCAGG TGGGCCGCCA CCCCCTGACC TGCCTGGGTC
>1815040	CAAAGACTGA GCCCTGCTGG
>1859374	CAAAGACTGA NCCCTGCTGG CGGACTTCAA GGAGAAGCCC CCACAGGGGA
Consensus	CAAAGACTGA GCCCTGCTGG CGGACTTCAA GGAGAAGCCC CCACAGGGGA
>1859374	TTTTGCTCCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG
>1650092	GGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG
Consensus	TTTTGCTCCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG
>1859374	GCCTTGTCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTCAGGACC
>1650092	GCCTTGTCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTCAGGACC
Consensus	GCCTTGTCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTCAGGACC
>1859374	ACCTTTGGGA GTGTCATCCT TACAAACCAC AGCATGCCCC GTCCTCCCA
>1650092	ACCTTTGGGA GTGTCATCCT TACAAACCAC AGCATGCCCC GTCCTCCCA
Consensus	ACCTTTGGGA GTGTCATCCT TACAAACCAC AGCATGCCCC GTCCTCCCA
>1859374	GAACCAGTCC CAGCCTGGGA GGATCAAGGC CTGGATCCCC GGCCGT
>1650092	GAACCAGTCC CAGCCTGGGA GGATCAAGGC CTGGATCCCC GGCCGT
Consensus	GAACCAGTCC CAGCCTGGGA GGATCAAGGC CTGGATCCCC GGCCGT
>1650092	CATCTGGAGG CTGCAGGGTC CTTGGGGTAA CAGGGACCAC
Consensus	CATCTGGAGG CTGCAGGGTC CTTGGGGTAA CAGGGACCAC

[illegible]

9885075
1512846
1551713
1251961
1209763
1815040
1859374
1650092

FIGURE 2

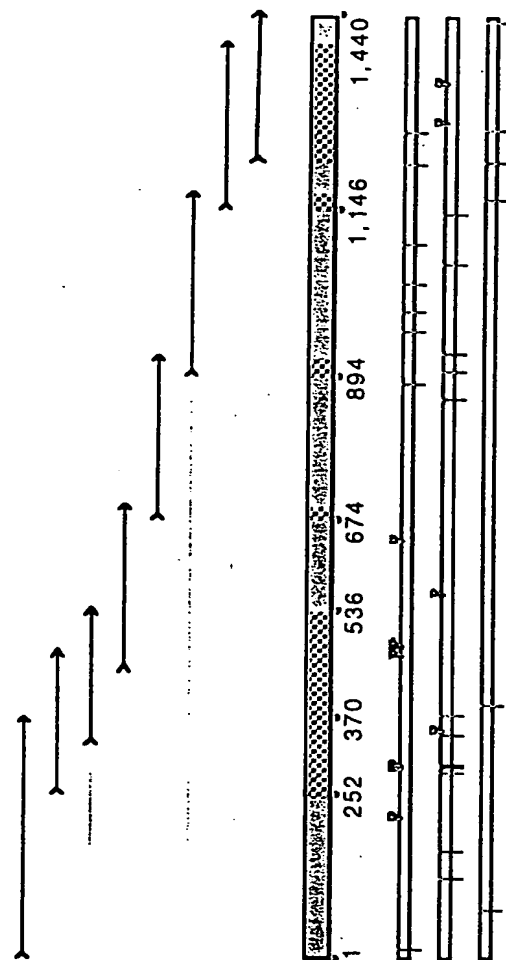
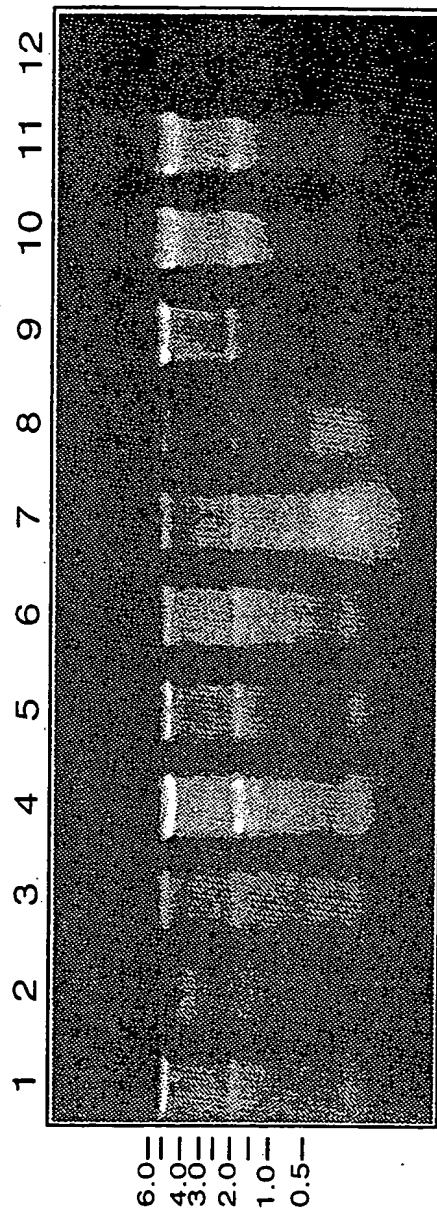


FIGURE 3A



Lane	Tissue
1	Bladder
2	Breast
3	Colon
4	Liver
5	Lung
6	Ovary
7	Placenta
8	Normal Prostate
9	Normal Prostate
10	Spleen
11	Testis
12	LnCap

CCST 200000

FIGURE 3B

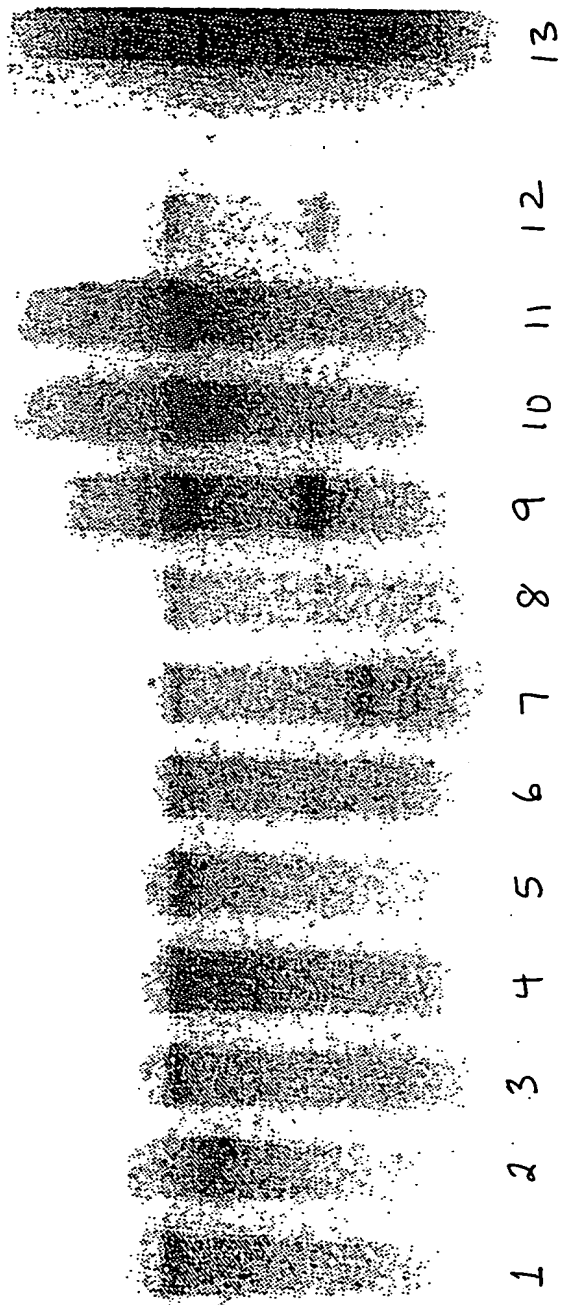


FIGURE 4A

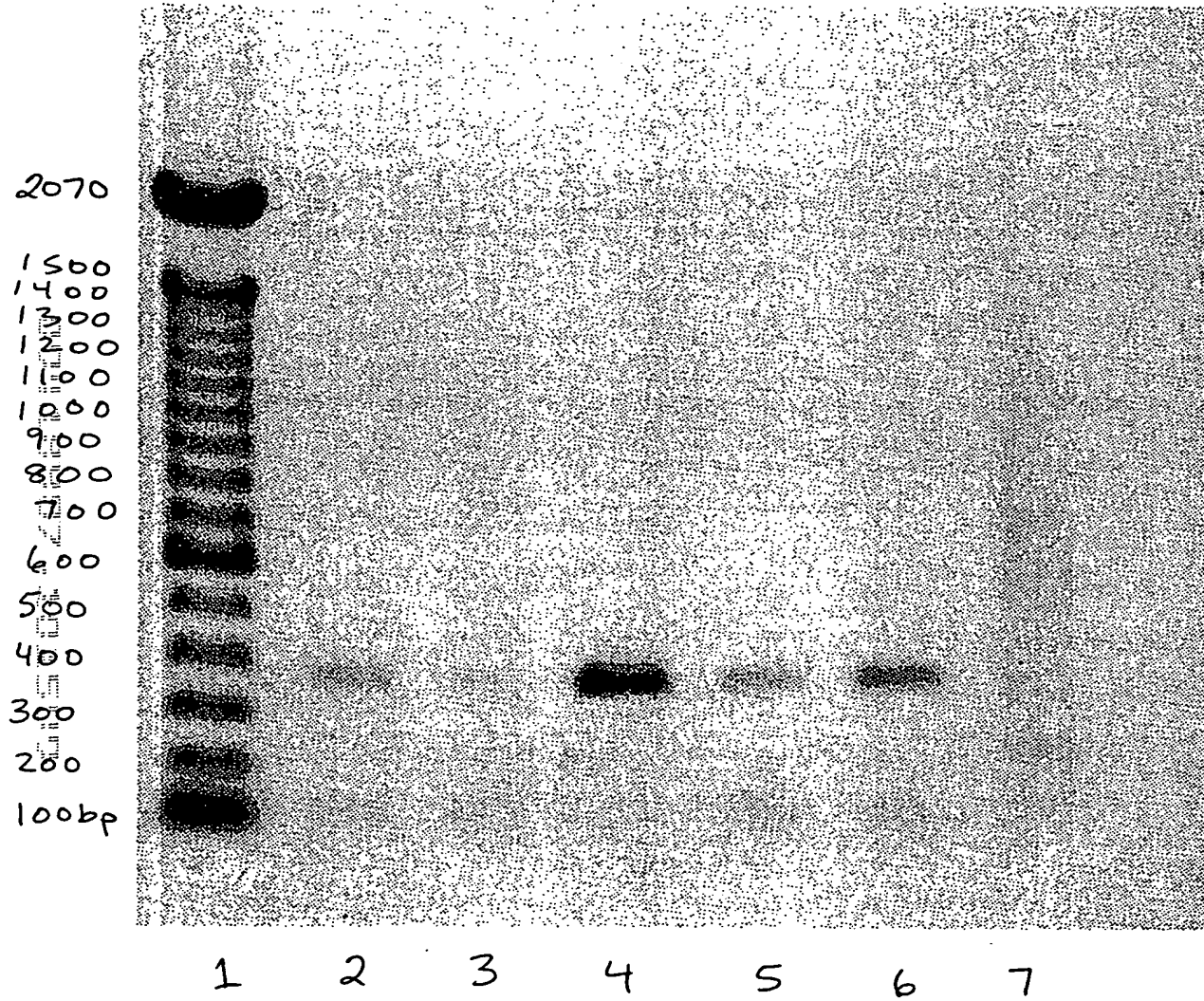


FIGURE 4B

